

In the Claims

1-43 (canceled).

44 (new). A composition of matter comprising:

- a) an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1;
- b) an isolated polynucleotide complementary to a messenger RNA transcribed from an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1;
- c) an isolated polynucleotide selected from the group consisting of:
 - (i) a polynucleotide comprising SEQ ID NO: 2;
 - (ii) a polynucleotide comprising SEQ ID NO: 52;
 - (iii) a polynucleotide comprising SEQ ID NO: 54;
 - (iv) a polynucleotide comprising SEQ ID NO: 55;
 - (v) an allelic variant of any of (i) to (iv) comprising at least one polymorphic variation compared to any of (i) to (iv) respectively, wherein said polymorphic variation is selected from the group consisting of UBP8rp-related biallelic markers Nos. 1 to 96;

Biallelic marker No.	Position on SEQ ID NO: 1	Alternative nucleotides
1	1199	A/G
2	1262	C/T
3	1426	C/G
4	1444	G/T
5	1487	A/G
6	1490	A/G
7	1505	G/T
8	1518	C/T
9	1554	C/T

Biallelic marker No.	Position on SEQ ID NO: 1	Alternative nucleotides
10	1630	A/G
11	1638	A/T
12	1680	A/G
13	1895	A/G
14	2180	A/G
15	2449	A/T
16	2721	G/T
17	3127	A/G
18	3137	C/T
19	3138	A/G
20	3183	A/G
21	3222	C/G
22	3269	C/T
23	3445	C/T
24	3470	A/G
25	3915	C/T
26	3973	A/C
27	4254	A/G
28	4472	A/T
29	4660	C/T
30	4770	A/G
31	4919	A/G
32	4973	C/T
33	5063	C/T
34	5065	G/T
35	5079	C/T
36	5080	C/T
37	5088	C/G
38	5090	C/T
39	5407	C/T
40	5466	A/G
41	5520	C/T
42	829	A/G
43	856	A/G
44	902	insertion of G
45	908	insertion of A
46	972	A/G
47	975	A/G
48	1006	C/T

Biallelic marker No.	Position on SEQ ID NO: 1	Alternative nucleotides
49	1018	A/G
50	1048	A/C
51	1056	C/T
52	1069	G/T
53	1073	A/G
54	1079	A/G
55	1108	A/G
56	1154	A/G
57	1181	A/G
58	1236	A/G
59	1263	A/G
60	1274	A/G
61	1319	G/T
62	1334	A/G
63	1444	G/T
64	1466	C/T
65	1489	A/G
66	1508	C/T
67	1521	G/T
68	1543	A/G
69	1687	A/C
70	1707	deletion of C
71	1728	A/G
72	1742	C/T
73	1810	C/T
74	1813	A/C
75	1841	C/T
76	1874	C/G
77	1875	A/G
78	1890	A/C
79	1907	A/G
80	1909	C/T
81	1921	A/C
82	1922	A/G
83	1957	A/G
84	1959	A/G
85	1976	C/T
86	1992	C/T
87	1993	C/T

Biallelic marker No.	Position on SEQ ID NO: 1	Alternative nucleotides
88	2096	C/G
89	2135	A/G
90	2192	A/G
91	2230	C/G
92	2275	C/T
93	2314	A/G
94	2370	A/C
95	2375	A/T
96	2525	C/T

- d) a polynucleotide complementary to any of (a) to (c);
- e) an isolated polypeptide encoded by:
 - (1) an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1;
 - (2) an isolated polynucleotide complementary to a messenger RNA transcribed from an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1; or
 - (3) an isolated polynucleotide selected from the group consisting of:
 - (i) a polynucleotide comprising SEQ ID NO: 2;
 - (ii) a polynucleotide comprising SEQ ID NO: 52;
 - (iii) a polynucleotide comprising SEQ ID NO: 54;
 - (iv) a polynucleotide comprising SEQ ID NO: 55;
 - (v) an allelic variant of any of (i) to (iv) comprising at least one polymorphic variation compared to any of (i) to (iv) respectively, wherein said polymorphic variation is selected from the group consisting of UBP8rp-related biallelic markers Nos. 1 to 96;
- f) an isolated polypeptide:
 - (i) comprising SEQ ID NO:3;

- (ii) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3;
- (iii) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3;
- (iv) an allelic variant of a polypeptide comprising SEQ ID NO:3; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3, said allelic variant comprising at least one polymorphic variation compared to any of said polypeptides respectively, wherein said polymorphic variation is encoded by a codon comprising a UBP8rp-related biallelic marker of the table set forth herein;
- (v) a mutein of a polypeptide comprising SEQ ID NO:3; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the sequences of said polypeptides;
- (vi) a mutein of a polypeptide comprising SEQ ID NO:3; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of said polypeptides under highly stringent conditions; or
- (vii) a mutein of a polypeptide comprising SEQ ID NO:3; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3,

wherein any changes in the amino acid sequence of said mutein are conservative amino acid substitutions of the amino acid sequences of said polypeptides;

- (viii) a polypeptide comprising SEQ ID NO:53;
- (ix) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53;
- (x) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3;
- (xi) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3 under highly stringent conditions; and
- (xiii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein any changes in the amino acid sequence of said mutein are

conservative amino acid substitutions of the amino acid sequences of said polypeptide;

- (xiv) a polypeptide comprising SEQ ID NO:56;
- (xv) a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56;
- (xvi) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56;
- (xvii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xviii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any one of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56 under highly stringent conditions; or
- (xix) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein any changes in the amino acid sequence of said mutein are

conservative amino acid substitutions of the amino acid sequence of said polypeptide;

- (g) an expression vector comprising:
 - A) an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1;
 - B) an isolated polynucleotide complementary to a messenger RNA transcribed from an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1; or
 - C) an isolated polynucleotide selected from the group consisting of:
 - (i) a polynucleotide comprising SEQ ID NO: 2;
 - (ii) a polynucleotide comprising SEQ ID NO: 52;
 - (iii) a polynucleotide comprising SEQ ID NO: 54;
 - (iv) a polynucleotide comprising SEQ ID NO: 55;
 - (v) an allelic variant of any of (i) to (iv) comprising at least one polymorphic variation compared to any of (i) to (iv) respectively, wherein said polymorphic variation is selected from the group consisting of UBP8rp-related biallelic markers Nos. 1 to 96; or
 - (vi) a polynucleotide complementary to any of (A) to (C);
- (h) a host cell comprising an expression vector comprising:
 - A) an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1;
 - B) an isolated polynucleotide complementary to a messenger RNA transcribed from an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1; or
 - C) an isolated polynucleotide selected from the group consisting of:

- (i) a polynucleotide comprising SEQ ID NO: 2;
 - (ii) a polynucleotide comprising SEQ ID NO: 52;
 - (iii) a polynucleotide comprising SEQ ID NO: 54;
 - (iv) a polynucleotide comprising SEQ ID NO: 55;
 - (v) an allelic variant of any of (i) to (iv) comprising at least one polymorphic variation compared to any of (i) to (iv) respectively, wherein said polymorphic variation is selected from the group consisting of UBP8rp-related biallelic markers Nos. 1 to 96; or
 - (vi) a polynucleotide complementary to any of (A) to (C); or
- (i) an isolated antibody that binds to a polypeptide comprising:
- (i) SEQ ID NO:3;
 - (ii) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3;
 - (iii) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3;
 - (iv) an allelic variant of any of (i) to (iii) comprising at least one polymorphic variation compared to any of (i) to (iii) respectively, wherein said polymorphic variation is encoded by a codon comprising a UBP8rp-related biallelic marker of the table set forth herein;
 - (v) a mutein of any of (i) to (iii), wherein the amino acid sequence has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the sequences in (i) to (iii);
 - (vi) a mutein of any of (i) to (iii) which is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of (i) to (iii) under highly stringent conditions; or
 - (vii) a mutein of any of (i) to (iii) wherein any changes in the amino acid sequence are conservative amino acid substitutions of the amino acid sequences in (i) to (iii);
 - (viii) a polypeptide comprising SEQ ID NO:53;

- (ix) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53;
- (x) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3;
- (xi) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3 under highly stringent conditions; and
- (xiii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein any changes in the amino acid sequence of said mutein are conservative amino acid substitutions of the amino acid sequences of said polypeptide;
- (xiv) a polypeptide comprising SEQ ID NO:56;

- (xv) a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56;
- (xvi) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56;
- (xvii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xviii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any one of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56 under highly stringent conditions; or
- (xix) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein any changes in the amino acid sequence of said mutein are conservative amino acid substitutions of the amino acid sequences in said polypeptide.

45 (new). The composition of matter according to claim 44, wherein the expression vector is a gene therapy vector.

46 (new). A method of making a polypeptide, said method comprising the steps of culturing a host cell under conditions suitable for the production of a polypeptide, said host cell comprising an expression vector comprising:

- A) an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1;
- B) an isolated polynucleotide complementary to a messenger RNA transcribed from an isolated gene comprising introns having a sequence of:
 - (i) nucleotides 1018 to 1046 of SEQ ID NO: 1; and
 - (ii) nucleotides 1676 to 1718 of SEQ ID NO: 1; or
- C) an isolated polynucleotide selected from the group consisting of:
 - (i) a polynucleotide comprising SEQ ID NO: 2;
 - (ii) a polynucleotide comprising SEQ ID NO: 52;
 - (iii) a polynucleotide comprising SEQ ID NO: 54;
 - (iv) a polynucleotide comprising SEQ ID NO: 55;
 - (v) an allelic variant of any of (i) to (iv) comprising at least one polymorphic variation compared to any of (i) to (iv) respectively, wherein said polymorphic variation is selected from the group consisting of UBP8rp-related biallelic markers Nos. 1 to 96; or
 - (vi) a polynucleotide complementary to any of (A) to (C);

47 (new). The method according to claim 46, further comprising the step of purifying said polypeptide from the culture.

48 (new). The method according to claim 47, further comprising the step of formulating said polypeptide into a pharmaceutical composition.

49 (new). A method of screening a polypeptide as a target for screening for natural binding partners or candidate modulators comprising contacting a polypeptide with a natural binding partner or a candidate modulator and measuring the activity of said polypeptide, said polypeptide comprising:

- (i) SEQ ID NO:3;
- (ii) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3;
- (iii) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3;
- (iv) an allelic variant of any of (i) to (iii) comprising at least one polymorphic variation compared to any of (i) to (iii) respectively, wherein said polymorphic variation is encoded by a codon comprising a UBP8rp-related biallelic marker of the table set forth herein;
- (v) a mutein of any of (i) to (iii), wherein the amino acid sequence has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the sequences in (i) to (iii);
- (vi) a mutein of any of (i) to (iii) which is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of (i) to (iii) under highly stringent conditions; or
- (vii) a mutein of any of (i) to (iii) wherein any changes in the amino acid sequence are conservative amino acid substitutions of the amino acid sequences in (i) to (iii);
- (viii) a polypeptide comprising SEQ ID NO:53;
- (ix) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53;
- (x) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3;

- (xi) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3 under highly stringent conditions;
- (xiii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein any changes in the amino acid sequence of said mutein are conservative amino acid substitutions of the amino acid sequences of said polypeptide;
- (xiv) a polypeptide comprising SEQ ID NO:56;
- (xv) a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56;
- (xvi) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56;

- (xvii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xviii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any one of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56 under highly stringent conditions; or
- (xix) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein any changes in the amino acid sequence of said mutein are conservative amino acid substitutions of the amino acid sequences in said polypeptide.

50 (new). The method according to claim 49, wherein said candidate modulator is selected from the group consisting of a natural ligand, a small molecule, an aptamer, an antisense mRNA, a small interfering RNA and an antibody.

51 (new). The method according to claim 49, wherein said modulator is a candidate drug for the treatment of a chronic inflammatory disease.

52 (new). The method according to claim 49, wherein the activity of said polypeptide is assessed by measuring the de-ubiquitinating activity of UBP8 in the presence of said polypeptide.

53 (new). A method of assessing the efficiency of a modulator of a polypeptide for the treatment of psoriasis, said method comprising administering said modulator to an animal model for psoriasis; wherein a determination that said modulator ameliorates a representative characteristic of psoriasis in said animal model indicates that said modulator is a drug for the treatment of psoriasis, said polypeptide comprising:

- (i) SEQ ID NO:3;
- (ii) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 3;
- (iii) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 3, wherein said span falls within amino acids 467 to 482 of SEQ ID NO: 3;
- (iv) an allelic variant of any of (i) to (iii) comprising at least one polymorphic variation compared to any of (i) to (iii) respectively, wherein said polymorphic variation is encoded by a codon comprising a UBP8rp-related biallelic marker of the table set forth herein;
- (v) a mutein of any of (i) to (iii), wherein the amino acid sequence has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the sequences in (i) to (iii);
- (vi) a mutein of any of (i) to (iii) which is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of (i) to (iii) under highly stringent conditions;
- (vii) a mutein of any of (i) to (iii) wherein any changes in the amino acid sequence are conservative amino acid substitutions of the amino acid sequences in (i) to (iii);

- (viii) a polypeptide comprising SEQ ID NO:53;
- (ix) a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53;
- (x) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3;
- (xi) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3 under highly stringent conditions;
- (xiii) a mutein of a polypeptide comprising SEQ ID NO:53; a polypeptide comprising a span of at least 470 amino acids of SEQ ID NO: 53; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 53, wherein said span falls within amino acids 467 to 485 of SEQ ID NO: 3, wherein any changes in the amino acid sequence of said mutein are conservative amino acid substitutions of the amino acid sequences of said polypeptide;
- (xiv) a polypeptide comprising SEQ ID NO:56;

- (xv) a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56;
- (xvi) a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56;
- (xvii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein the amino acid sequence of said mutein has at least 95%, 96%, 97%, 98% or 99% identity to at least one of the polypeptide sequences;
- (xviii) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, which mutein is encoded by a nucleic acid which hybridizes to the complement of a DNA sequence encoding any one of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56 under highly stringent conditions; or
- (xix) a mutein of a polypeptide comprising SEQ ID NO:56; a polypeptide comprising a span of at least 270 amino acids of SEQ ID NO: 56; or a polypeptide comprising a span of at least 15 amino acids of SEQ ID NO: 56, wherein said span comprises amino acids 266 and 267 of SEQ ID NO: 56, wherein any changes in the amino acid sequence of said mutein are conservative amino acid substitutions of the amino acid sequences in said polypeptide.

54 (new). The method according to claim 53, wherein said representative characteristic is a Psoriasis Area and Severity Index score.

55 (new). The method according to claim 54, wherein a 75% or greater improvement in Psoriasis Area and Severity Index scores (PASI 75) indicates that said modulator is a drug for the treatment of psoriasis.

56 (new). The method according to claim 53, wherein said animal model is a SCID-hu Mouse.

57 (new). A method of genotyping comprising the steps of:

- a) isolating a nucleic acid from a biological sample; and
- b) detecting the nucleotide present at one or more of the UBP8rp-related biallelic markers selected from the group consisting of biallelic markers Nos. 1, 2, 4, 6, 7, 10, 12-19, 21-30, 31-35 and 37-96.

58 (new). The method according to claim 57, wherein said biological sample is derived from a single individual.

59 (new). The method according to claim 58, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said individual's genome.

60 (new). The method according to claim 57, wherein said determining is performed by a microsequencing assay.

61 (new). The method according to claim 57, further comprising amplifying a portion of a sequence comprising the biallelic marker prior to said determining step.

62 (new). The method according to claim 61, wherein said amplifying is performed by PCR.

63 (new). The method according to claim 57, further comprising the step of correlating the result of the genotyping steps with a risk of suffering from a chronic inflammatory disease.

64 (new). The method according to claim 63, wherein the presence of allele A9 in said individual indicates that said individual suffers from or is at risk of suffering from said chronic inflammatory disease.

65 (new). The method according to claim 64, wherein said chronic inflammatory disease is psoriasis.